

U99798680980 500

RTA	IFPKQYPIINFITTAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRVG	50
GELONIN	GLD-----TVSFSTKGATYITYVNFNLNLRVKLKPEGN-SHGIPLLRKKCD	45
RTA	LPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNOED	100
GELONIN	DP-GKCFVLVALSNDNGQLAEIAIDVTSVYVVGQVRNRSYFF----KDA	90
RTA	AEAITHLFTDVONRYTFAFGGNYDRLEQLAGNLRENIELGNPLEEAISA	150
GELONIN	PDAAYEGLFKNTIKTRLHFGSTYPSLEG-EKAYRETTDLGIEPLRIGIKK	139
RTA	LYYSTGGTQLPTLARSFIICIONISEAARFQYIEGEMRTRIRYNRRSAP	200
GELONIN	LDENAIQNYKPTIEASSLLVVIONVSEARFTFIENQIRNN--FQQRIRP	187
RTA	DPSVITLENSWGRSLTAIQESN-QGAFASPIQLQRRNGSKFSYDVVSILI	249
GELONIN	ANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTVADQVK	237
RTA	PIIALMWYRCAPPPSSQF	267
GELONIN	PKIALLKFFVDKDPK	251

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RTA	I-----FPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVREIPV	44
BRIP	AAKMAKNVDKPLFTATFNVOASSAD-YATFIAGIRNKLNPAPHFSNRPV	49
RTA	LPN-RVGLPINORFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFF	93
BRIP	LPPVEPNVPPSRWFHVVLKASPTSAGLTLAIRADNIYLEGFKSSDGTWME	99
RTA	HPDNOEDAEAIHTLFTDVONRYTFAFGGNYDRLEQLAGNLRENIELGNP	143
BRIP	LTPGLIPGATYV-----GFGGTYRDLLGDTDKL-TNVALGRQQ	136
RTA	LEEASALY-----YYSTGGTOLPTLARSFIICIMISEAARFQ-----YIE	185
BRIP	LADAVTALHGRTKADKASGPKQQQAREAVTTLLVMVNEATRFQTVSGFVA	186
RTA	GEMRTRIRYNRRSAPDPSVITLENSWGRSLTAIQESNOGAFASPIQLORR	235
BRIP	GLLHPKAVEKSKGKIGNEMKAQVNGWQDLAALLKTDVKPPPGKSPAKFA	236
RTA	NGSKFSVYDVSILIPITIALMVYRCAP-----PPSSQF	267
BRIP	PIEKMVGVRTAEQAANTLGILLFVEVPGGLTVAKALELFHASGGK	280

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RTA	IFPKQYPIINF	TAGATVQSYTNF	IRAVRGRLTTGADVRHEIPVLPNRVG	50
LUFFIN	D-----	VRFSLSGSSTS	YSKFIGDLRKALPSNGTVYNLTILLSSASG	43
RTA	LPINORFILVEL	SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQED	100	
LUFFIN	---	ASRYTLMTSLSNYDGKAITVAVDVSQLYINGYLVNSTSYFF---	NESD 87	
RTA	AEAITHLFTDVQ	NRYTFAFGGNYDRLEQLAGNLRENIELGNGLPEEAISA	150	
LUFFIN	AKLASQYVFKG	STIVTLPYSGNYEKLQTAAGKIREKIPGLGFPALDSALTT	137	
RTA	LYYYSTGGTQ	PTLARSFIICIONISEAARFQYIEGEMTRIRYNRRSAP	200	
LUFFIN	IFHYDSTAA----	AAAFVLVILQTTAEASRFKYIEGQIIERI--SKNQVP	180	
RTA	DPSVITLENS-	WGRNSTAIQ--ESNOGAFASPIQLORRNGSKFSVYDVS	247	
LUFFIN	SLATISLENSL	WSALSQIQLAOTNNGTFTKTPVITDDKQORVEITNVT	230	
RTA	LIPITIALMV	RYCAPPPSSQF	267	
LUFFIN	KVVTKNIQ	LLLLNYKONVA	248	

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RTA	IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVG	50
MAP	A-PTLETIASLDLNNPT--TYLSFITNIRTKVADKTE-----OCTIQKIS	42
RTA	LPINQRFILVELSNHAELSVTLALDVTNAYVVGYRA---GNSAYFFHPDN	97
MAP	KTFTQRYSYIDLIVSSTOKITLAIMDADLYVLGYSDIANNKGRAFFFKOV	92
RTA	QEDAEATHLFTDVQNRYYTFAFGGNYDRLEQLAGNLRENIELGNPLEEA	147
MAP	TEAVANNFFPGATGTNRIKLT*TTGSYGDEK-NGGLRKDNPLGIFRLENS	141
RTA	ISALYYYSTGGTQLPTLARSFIICIONISEAARFQYIEGEMTRIRYNRR	197
MAP	IVNIY---GKAGDVKKOAKFFLLAIOMVSEAAARFKYI-SDKIPSEKYEE-	186
RTA	SAPDPSVITLENSWGRSLTAIQESNOGAFASPIQLORRNGSKFSYVDVSI	247
MAP	VTVDYMTALENNWAKLSTAVYNSKPSTTTATKCOLATSPVTISPWIFKT	236
RTA	LIPITIALMVYRCAPPPSSQF	267
MAP	VEEIKLVMGLLKSS	250

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RTA	IFPKQYPIINFITTAGATVQSYTNFIRAVRGRLLTTGADVRHEIPVLPNRVG	50
PAPS	I-----NTITFDAGNATINKYATFMESLRNEAKDPSLKCYGIPMLPNTNS	45
RTA	LPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSA-----YFFHP	95
PAPS	---TIKYLKLGASLKTITLMLRRNLYVMGYSDPYDNKCRYHIFNDI	92
RTA	DNQEDAEAITHLFTDVONRYT--FAFGGNYDRLEQLAG--NLRENIELGNG	142
PAPS	KGTEYSDVENTLCPSSNPRVAKPINYNGLYPTLEKKAGVTSRNEVOLGIQ	142
RTA	PLEEIASALYYSTGGTQPLTLARSFIICIONISEAARFQYIEGEMRTI	192
PAPS	ILSSDIGKI--SGGGSFTEKIEAKFLVAIQMVSEAARFKYIENQVKTN-	189
RTA	RYNRRSAPDPSVITLENSWGRSLTAIQESNOGAFASPIQLORRNGSKFSV	242
PAPS	-FNRDFSPNDKVLDLEENWGKISTAIHNSKNGALPKPLELKNADGTKWIV	238
RTA	YDVSILIPIIIALMVYRCAPPPSSQF	267
PAPS	LRVDEIKPDVGLLNY--VNGTCOAT	261

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HUH-G3
GCA GCT TCT GGG TAT ACC TTC ACA AAC TAT GGA ATG AAC TGG GTG AAG CAG GCT CCA GGA AAG
GGT TTA AGG TGG ATG GGC TGG

HUH-G4
AAA GAG AAG GTA AAC CGT CCC TTG AAG TC A TCA GCA TAT GTT GGC TCT CCA GTG TGG GTG TTT
ATC CAG CCC ATC CAC CTT AAA C

HUH-G5
GAC GGT TTA CCT TCT TGG ACA CGT CTA AGT GCA CTG CCT ATT TAC AGA TCA ACA GCCTCA GAG
CCG AGG ACA CGG CTA CAT

HUH-G6
AGG AGA CGG TGA CCG TGG TCC CTT GGC CCC AGA CAT CGA AGT ACC AGT AAC CCC GTC TTG
TAC AGA AAT ATG TAG CCG TGT CCT CGG C

H65G-2S
ACT AGT GTC GAC ATC ATG GCT TGG GT

H65-G2
GAG GAG ACG GTG ACC GTG GT

H65K-2S
AGT CGT CGA CAC GAT GGA CAT GAG GAC

JK1-HindIII
GTT TGA TTT CAA GCT TGG TGC

